GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 01:06:58 ; Search time 755.06 Seconds
(without alignments)
28.386 Million cell updates/sec

Title: US-09-851-670-12
Perfect score: 25
Sequence: 1 acagctcgcccccattaacatattc 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1026190

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_1101:*
1: /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	14.6	58.4	31	20	AAX39404	Human genomic DNA
	2	14.6	58.4	31	20	AAX39251	Human genomic DNA
	3	14.6	58.4	31	20	AAX39268	Human genomic DNA
	4	14.6	58.4	31	20	AAX39115	Human genomic DNA
c	5	14	56.0	50	22	AAF76756	T flavus promoter
	6	13.8	55.2	33	21	AAA30367	Plasmid TKHH2 PCR
	7	13.6	54.4	40	19	AAV64245	Plasmid pPK7/8 pri
	8	13.6	54.4	47	21	AAZ68336	Human map-related
c	9	13.6	54.4	50	21	AAA65647	Bacillus subtilis
	10	13.4	53.6	20	20	AAX36656	PCR primer for mar
	11	13.4	53.6	29	21	AAA73281	A. fumigatus 13073
	12	13.4	53.6	29	21	AAZ59726	Aspergillus fumiga
c	13	13.4	53.6	29	21	AAZ59727	Aspergillus fumiga
	14	13.4	53.6	29	22	AAS05802	A. fumigatus site
c	15	13.4	53.6	29	22	AAS05803	A. fumigatus site
c	16	13.4	53.6	36	18	AAV09734	Adenovirus minigen
	17	13.4	53.6	58	18	AAT90696	Primer #1 for env
c	18	13.4	53.6	59	20	AAX77264	Hepatitis B virus
c	19	13.4	53.6	59	20	AAX77265	Hepatitis B virus
	20	13.2	52.8	34	17	AAT33916	Human G-protein co
	21	13.2	52.8	34	18	AAT43397	Primer #3 for G-pr
	22	13.2	52.8	34	21	AAA70784	Primer #1 for huma
	23	13.2	52.8	34	21	AAZ60132	PCR primer #13 use
	24	13	52.0	36	18	AAV09733	Adenovirus minigen
	25	13	52.0	51	22	AAH79919	Human DNA containi
c	26	12.8	51.2	22	19	AAV11151	Oligonucleotide #4
c	27	12.6	50.4	20	18	AAV25233	Primer F3 for H.py
c	28	12.6	50.4	20	21	AAA98290	Human MSH6 fragmen
	29	12.6	50.4	22	20	AAZ09089	Lambda gt10 revers
	30	12.6	50.4	22	20	AAX89280	PDE8A specific pri
	31	12.6	50.4	22	21	AAA72007	Lambda-gt10 revers
	32	12.6	50.4	32	19	AAV00603	Anti-human SC sing
	33	12.6	50.4	32	21	AAA75891	PCR primer used to
	34	12.6	50.4	32	21	AAA61406	Murine anti-human
	35	12.6	50.4	36	22	AAS09503	Humanised anti-p18
	36	12.6	50.4	41	19	AAV51007	Maize polymorphic
	37	12.6	50.4	41	19	AAV51000	Maize polymorphic
c	38	12.6	50.4	42	21	AAZ96605	T cell antigen rec
	39	12.6	50.4	50	22	AAF76757	T flavus promoter
c	40	12.6	50.4	59	21	AAA62670	Cry2A family gene
	41	12.4	49.6	19	21	AAZ70966	Human biallelic ma
c	42	12.4	49.6	19	21	AAZ72626	Human biallelic ma
	43	12.4	49.6	21	12	AAQ14323	MCPC 603 VL CDR2 w
	44	12.4	49.6	21	19	AAV60865	Mutagenic oligonuc
	45	12.4	49.6	23	20	AAZ25795	Expression plasmid

ALIGNMENTS

RESULT 1
AAX39404
ID AAX39404 standard; DNA; 31 BP.
XX
AC AAX39404;
XX
DT 15-JUN-1999 (first entry)
XX
DE Human genomic DNA polymorphic site sequence tag 851.
XX
KW Polymorphic site; human; forensic; paternity testing; phenotypic trait;
KW diagnosis; disease susceptibility; autoimmune disease; infection; cancer;
KW inflammatory disorder; nervous system disorder; longevity; drug response;
KW physical characteristic; therapy; breeding program; linkage; locus;
KW gene mapping; treatment; prevention; ss.
XX
OS Homo sapiens.
XX
PN WO9914228-A1.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-US19325.
XX
PR 18-NOV-1997; 97US-0066172.
PR 17-SEP-1997; 97US-0059304.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Berno A, Chee M, Fan J, Lipshutz RJ;
XX
DR WPI; 1999-229497/19.
XX
PT Nucleic acid encoding specific human polymorphisms

XX
PS Claim 1; Page 23; 56pp; English.
XX
CC This invention describes nucleic acid segments represented in
CC AAX38554-X39408 which are isolated from any of about 750 human genomic
CC regions given in the specification that include a polymorphic site, or
CC their complements. Analysis of the polymorphisms is useful (1) to
CC identify individuals for forensic studies and paternity testing, (2) to
CC correlate the polymorphisms with phenotypic traits, e.g. for diagnosis
CC of, or susceptibility to, a wide range of diseases including autoimmune,
CC inflammatory and nervous system disorders, cancer, infections etc., also
CC longevity, physical characteristics, response to drugs or therapy, also
CC in animals and plants to identify individuals for breeding programs, (3)
CC to identify physical linkage between nucleic acid segments and a
CC specific genetic locus, associated with a trait for gene mapping and for
CC subsequent cloning of the gene responsible for the trait. The products
CC of the invention may also be used for treatment or prevention of the
CC specified diseases.
XX
SQ Sequence 31 BP; 11 A; 10 C; 4 G; 5 T; 1 other;

Query Match 58.4%; Score 14.6; DB 20; Length 31;
Best Local Similarity 73.9%; Pred. No. 4.4e+02;
Matches 17; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 acagctcgcccccattaacatat 23
|||||| |||: || ||||| ||
Db 7 acagcacgcygacactaacacat 29

RESULT 2
AAX39251
ID AAX39251 standard; DNA; 31 BP.
XX
AC AAX39251;
XX
DT 15-JUN-1999 (first entry)
XX
DE Human genomic DNA polymorphic site sequence tag 698.
XX
KW Polymorphic site; human; forensic; paternity testing; phenotypic trait;
KW diagnosis; disease susceptibility; autoimmune disease; infection; cancer;
KW inflammatory disorder; nervous system disorder; longevity; drug response;
KW physical characteristic; therapy; breeding program; linkage; locus;
KW gene mapping; treatment; prevention; ss.
XX
OS Homo sapiens.
XX
PN WO9914228-A1.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-US19325.
XX
PR 18-NOV-1997; 97US-0066172.
PR 17-SEP-1997; 97US-0059304.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Berno A, Chee M, Fan J, Lipshutz RJ;
XX
DR WPI; 1999-229497/19.
XX
PT Nucleic acid encoding specific human polymorphisms
XX
PS Claim 1; Page 21; 56pp; English.
XX
CC This invention describes nucleic acid segments represented in
CC AAX38554-X39408 which are isolated from any of about 750 human genomic
CC regions given in the specification that include a polymorphic site, or
CC their complements. Analysis of the polymorphisms is useful (1) to
CC identify individuals for forensic studies and paternity testing, (2) to
CC correlate the polymorphisms with phenotypic traits, e.g. for diagnosis
CC of, or susceptibility to, a wide range of diseases including autoimmune,
CC inflammatory and nervous system disorders, cancer, infections etc., also
CC longevity, physical characteristics, response to drugs or therapy, also
CC in animals and plants to identify individuals for breeding programs, (3)
CC to identify physical linkage between nucleic acid segments and a
CC specific genetic locus, associated with a trait for gene mapping and for
CC subsequent cloning of the gene responsible for the trait. The products
CC of the invention may also be used for treatment or prevention of the
CC specified diseases.
XX
SQ Sequence 31 BP; 11 A; 10 C; 4 G; 5 T; 1 other;

Query Match 58.4%; Score 14.6; DB 20; Length 31;
Best Local Similarity 73.9%; Pred. No. 4.4e+02;
Matches 17; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 acagctcgcccccattaacatat 23
|||||| |||: || ||||| ||
Db 7 acagcacgcygacactaacacat 29

RESULT 3
AAX39268
ID AAX39268 standard; DNA; 31 BP.
XX
AC AAX39268;
XX
DT 15-JUN-1999 (first entry)
XX
DE Human genomic DNA polymorphic site sequence tag 715.
XX
KW Polymorphic site; human; forensic; paternity testing; phenotypic trait;
KW diagnosis; disease susceptibility; autoimmune disease; infection; cancer;
KW inflammatory disorder; nervous system disorder; longevity; drug response;
KW physical characteristic; therapy; breeding program; linkage; locus;
KW gene mapping; treatment; prevention; ss.
XX
OS Homo sapiens.
XX
PN WO9914228-A1.
XX
PD 25-MAR-1999.
XX
PF 16-SEP-1998; 98WO-US19325.
XX
PR 18-NOV-1997; 97US-0066172.
PR 17-SEP-1997; 97US-0059304.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Berno A, Chee M, Fan J, Lipshutz RJ;
XX
DR WPI; 1999-229497/19.
XX
PT Nucleic acid encoding specific human polymorphisms
XX
PS Claim 1; Page 21; 56pp; English.
XX
CC This invention describes nucleic acid segments represented in
CC AAX38554-X39408 which are isolated from any of about 750 human genomic
CC regions given in the specification that include a polymorphic site, or
CC their complements. Analysis of the polymorphisms is useful (1) to
CC identify individuals for forensic studies and paternity testing, (2) to
CC correlate the polymorphisms with phenotypic traits, e.g. for diagnosis
CC of, or susceptibility to, a wide range of diseases including autoimmune,
CC inflammatory and nervous system disorders, cancer, infections etc., also
CC longevity, physical characteristics, response to drugs or therapy, also
CC in animals and plants to identify individuals for breeding programs, (3)
CC to identify physical linkage between nucleic acid segments and a
CC specific genetic locus, associated with a trait for gene mapping and for
CC subsequent cloning of the gene responsible for the trait. The products

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CC   of the invention may also be used for treatment or prevention of the
CC   specified diseases.
XX
SQ   Sequence 31 BP; 11 A; 10 C; 4 G; 5 T; 1 other;


  Query Match             58.4%;  Score 14.6;  DB 20;  Length 31;
  Best Local Similarity   73.9%;  Pred. No. 4.4e+02;
  Matches   17;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1 acagctcgcccccattaacatat 23
           ||||| |||:  || ||||| ||
Db       7 acagcacgcygacactaacacat 29


RESULT   4
AAX39115
ID   AAX39115 standard; DNA; 31 BP.
XX
AC   AAX39115;
XX
DT   15-JUN-1999  (first entry)
XX
DE   Human genomic DNA polymorphic site sequence tag 562.
XX
KW   Polymorphic site; human; forensic; paternity testing; phenotypic trait;
KW   diagnosis; disease susceptibility; autoimmune disease; infection; cancer;
KW   inflammatory disorder; nervous system disorder; longevity; drug response;
KW   physical characteristic; therapy; breeding program; linkage; locus;
KW   gene mapping; treatment; prevention; ss.
XX
OS   Homo sapiens.
XX
PN   WO9914228-A1.
XX
PD   25-MAR-1999.
XX
PF   16-SEP-1998;   98WO-US19325.
XX
PR   18-NOV-1997;   97US-0066172.
PR   17-SEP-1997;   97US-0059304.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Berno A,  Chee M,  Fan J,  Lipshutz RJ;
XX
DR   WPI; 1999-229497/19.
XX
PT   Nucleic acid encoding specific human polymorphisms
XX
PS   Claim 1; Page 18; 56pp; English.
XX
CC   This invention describes nucleic acid segments represented in
CC   AAX38554-X39408 which are isolated from any of about 750 human genomic
CC   regions given in the specification that include a polymorphic site, or
CC   their complements. Analysis of the polymorphisms is useful (1) to
CC   identify individuals for forensic studies and paternity testing, (2) to
CC   correlate the polymorphisms with phenotypic traits, e.g. for diagnosis
CC   of, or susceptibility to, a wide range of diseases including autoimmune,
CC   inflammatory and nervous system disorders, cancer, infections etc., also
CC   longevity, physical characteristics, response to drugs or therapy, also
CC   in animals and plants to identify individuals for breeding programs, (3)
CC   to identify physical linkage between nucleic acid segments and a
CC   specific genetic locus, associated with a trait for gene mapping and for
CC   subsequent cloning of the gene responsible for the trait. The products
CC   of the invention may also be used for treatment or prevention of the
CC   specified diseases.
XX
SQ   Sequence 31 BP; 11 A; 10 C; 4 G; 5 T; 1 other;


  Query Match             58.4%;  Score 14.6;  DB 20;  Length 31;
  Best Local Similarity   73.9%;  Pred. No. 4.4e+02;
  Matches   17;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1 acagctcgcccccattaacatat 23
           ||||| |||:  || ||||| ||
Db       7 acagcacgcygacactaacacat 29


RESULT   5
AAF76756/c
ID   AAF76756 standard; DNA; 50 BP.
XX
AC   AAF76756;
XX
DT   17-MAY-2001  (first entry)
XX
DE   T flavus promoter sequence #7.
XX
KW   Thermophile; promoter; terminator; thermophilic gene expression;
KW   fermentation; mesophilic gene thermostability; ds.
XX
OS   Thermus flavus.
XX
PN   WO200118217-A2.
XX
PD   15-MAR-2001.
XX
PF   06-SEP-2000; 2000WO-US24430.
XX
PR   07-SEP-1999;   99US-0390867.
XX
PA   (THER-) THERMOGEN INC.
XX
PI   Peredeltchouk M,  Vonstein V,  Demirjian D;
XX
DR   WPI; 2001-226747/23.
XX
PT   Isolated recombinant DNA molecule for identification of a regulatory
PT   region, e.g. a thermophile promoter, comprises a putative thermophile
PT   promoter operably linked to a reporter sequence, a drug resistance
PT   marker and a targeting sequence
XX
PS   Claim 15; Page 41; 44pp; English.
XX
CC   The present invention provides DNA sequences for identification of
CC   regulatory regions of a thermophile genome, comprising a reporter,
CC   promoter and drug resistance gene. Also provided are the sequences of
CC   several thermophile promoter and terminator sequences. These are useful
CC   for expressing thermophilic genes, such as those encoding enzymes, in the
CC   production of fermentation strains for high-temperature bioprocesses,
CC   and to enable the thermostabilisation of mesophilic genes.
XX
SQ   Sequence 50 BP; 16 A; 11 C; 8 G; 15 T; 0 other;


  Query Match             56.0%;  Score 14;  DB 22;  Length 50;
  Best Local Similarity   77.3%;  Pred. No. 9.4e+02;
  Matches   17;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1 acagctcgcccccattaacata 22
           | ||||||| || |||||| |
Db      22 AAAGCTCGCTTCCTTTAACAAA 1


RESULT   6
AAA30367
ID   AAA30367 standard; DNA; 33 BP.
XX
AC   AAA30367;
XX
DT   05-SEP-2000  (first entry)
XX
DE   Plasmid TKHH2 PCR primer MF26.
XX
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KW   Proteomics; DNA vaccination; mRNA vaccination; antibody production;
KW   PCR primer; ss.
XX
OS   Hepatitis B virus.
XX
PN   WO200029444-A1.
XX
PD   25-MAY-2000.
XX
PF   12-NOV-1999;   99WO-US26843.
XX
PR   16-NOV-1998;   98US-0108487.
XX
PA   (GENW-) GENWAY BIOTECH INC.
PA   (DUAN/) DUAN L.
XX
PI   Duan L;
XX
DR   WPI; 2000-387749/33.
XX
PT   Generation of antibodies in an avian species, for use in functional
PT   analysis of proteins, by vaccination with DNA encoding the antigen
PT   operably linked to a suitable promoter -
XX
PS   Example 5; Page 37; 83pp; English.
XX
CC   The present sequence is a PCR primer for plasmid pTKHH2, which was used
CC   in the construction of hepatitis B polymerase gene expression vector,
CC   which was then used to vaccinate chickens. This enabled the production of
CC   antibodies which can be used in the functional analysis of proteins
CC   (proteomics).
XX
SQ   Sequence 33 BP; 9 A; 13 C; 5 G; 6 T; 0 other;
```

```
  Query Match             55.2%;  Score 13.8;  DB 21;  Length 33;
  Best Local Similarity   72.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       1 acagctcgcccccattaacatattc 25
           | ||||||||| ||||   | ||| |
Db       2 agagctcgccaccatggccctatcc 26
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```
RESULT   7
AAV64245
ID   AAV64245 standard; DNA; 40 BP.
XX
AC   AAV64245;
XX
DT   25-JAN-1999  (first entry)
XX
DE   Plasmid pPK7/8 primer PK8.
XX
KW   Antimycotic agent; target; medicine; infection; veterinary; fungicide;
KW   immunodepression; preservative; food industry; fungi; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9844135-A2.
XX
PD   08-OCT-1998.
XX
PF   02-APR-1998;   98WO-EP01904.
XX
PR   02-APR-1997;   97DE-1013572.
XX
PA   (FARH ) HOECHST AG.
XX
PI   Entian K,  Feldmann H,  Hegemann J,  Hinnen A,  Koetter P;
PI   Kramer W,  Munder T,  Rose M,  Schuster T,  Zimmermann FK;
XX
DR   WPI; 1998-557125/47.
XX
PT   Identification of antimycotic agents using essential fungal proteins
PT   or genes as targets - useful, e.g. for potential clinical, human or
PT   veterinary medicine, for treatment of existing infections and for
PT   prevention of these in immune depressed subjects
XX
PS   Example 4; Page 32; 76pp; German.
XX
CC   AAV64240-V64253 are primers used in a method for the identification of
CC   antimycotic agents using as a target a nucleic acid which controls an
CC   essential protein of Saccharomyces cerevisiae or from other species of
CC   Mycetes. Such agents are potentially useful clinically, in human or
CC   veterinary medicine, for treating existing infections and for preventing
CC   them in immune-depressed subjects (those with human immune deficiency
CC   virus infection or diabetes), also as fungicides and preservatives for
CC   foods and body care products. The agents are used to identify equivalent
CC   genes in other fungi, specifically Candida albicans or Aspergillus
CC   fumigatus, and equivalent human, animal and plant genes, and also for
CC   identification of antimycotic agents..
XX
SQ   Sequence 40 BP; 9 A; 13 C; 7 G; 11 T; 0 other;
```

```
  Query Match             54.4%;  Score 13.6;  DB 19;  Length 40;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       6 tcgcccccattaacatattc 25
           ||  ||| || |||||||||
Db      17 tctaccctatgaacatattc 36
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```
RESULT   8
AAZ68336
ID   AAZ68336 standard; DNA; 47 BP.
XX
AC   AAZ68336;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human map-related biallelic marker SEQ ID NO:2683.
XX
KW   Human genome; biallelic marker; high density disequilibrium map;
KW   genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW   haplotyping; hybridisation; identification; characterisation;
KW   diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(24,A)
FT                   /*tag= a
FT                   /standard_name= "single nucleotide polymorphism"
XX
PN   WO9954500-A2.
XX
PD   28-OCT-1999.
XX
PF   21-APR-1999;   99WO-IB00822.
XX
PR   21-APR-1998;   98US-0082614.
PR   23-NOV-1998;   98US-0109732.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I;
XX
DR   WPI; 2000-013267/01.
XX
PT   Novel biallelic markers used to construct a high density disequilibrium
PT   map of the human genome -
XX
PS   Claim 3; Page 802; 2745pp; English.
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XX
CC   AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC   invention, which contain a polymorphic base at position 24 of their
CC   nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC   primers for the biallelic markers. The biallelic markers of the
CC   invention have a variety of uses: they can be used for high density
CC   mapping of the human genome, and in complex association studies and
CC   haplotyping studies which are useful in determining the genetic basis
CC   for disease states. Compositions and methods of the invention can also
CC   be useful for the identification of the targets for the development of
CC   pharmaceutical agents and diagnostic methods, as well as the
CC   characterisation of the differential efficacious responses to and side
CC   effects from pharmaceutical agents acting on a disease as well as other
CC   treatment.
CC   N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC   and 3367, are not actually given a sequence in the Sequence Listing
CC   from the present invention.
XX
SQ   Sequence 47 BP; 10 A; 14 C; 7 G; 16 T; 0 other;


  Query Match             54.4%;  Score 13.6;  DB 21;  Length 47;
  Best Local Similarity   80.0%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       5 ctcgccccccattaacatatt 24
           ||  |||||| |||||| ||
Db       1 ctttcccccaataacatgtt 20


RESULT   9
AAA65647/c
ID   AAA65647 standard; DNA; 50 BP.
XX
AC   AAA65647;
XX
DT   14-NOV-2000  (first entry)
XX
DE   Bacillus subtilis subtilase mutagenic PCR primer #3.
XX
KW   Subtilase; I-S1; I-S2; variant; detergent; laundry; dishwashing;
KW   leather industry; skin depilation; wool industry; cleaning;
KW   wash performance; mutagenesis; PCR primer; ss.
XX
OS   Bacillus subtilis.
XX
PN   WO200037623-A1.
XX
PD   29-JUN-2000.
XX
PF   20-DEC-1999;   99WO-DK00713.
XX
PR   18-DEC-1998;   98DK-0001675.
XX
PA   (NOVO ) NOVO-NORDISK AS.
XX
PI   Andersen Vilbour K,  Mikkelsen F,  Hansen Kamp P,  Andersen C;
PI   Norregaard-Madsen M;
XX
DR   WPI; 2000-452184/39.
XX
PT   Variant of subtilase enzyme of I-S1 and I-S2 sub-groups useful in
PT   laundry and/or dishwash detergent, comprises one additional amino acid
PT   residue at position 96 in active site loop region from position 95-103
PT   -
XX
PS   Example; Page 45; 72pp; English.
XX
CC   The present invention describes an isolated subtilase enzyme (I) of I-S1
CC   and I-S2 sub-groups having one additional amino acid residue at position
CC   96 in active site loop (b) region from position 95-103, between 96 and
CC   97. (I) and compositions comprising (I) are useful in laundry and/or
CC   dishwash detergent. (I) is used in the leather industry especially for
CC   depilation of skins, and in wool industry especially for cleaning wool
CC   clothes. Unlike the parent subtilase enzyme, the variant subtilase
CC   has improved wash performance. The present sequence represents a
CC   mutagenic PCR primer for subtilase, which is used in an example from
CC   the present invention.
XX
SQ   Sequence 50 BP; 9 A; 10 C; 16 G; 12 T; 3 other;


  Query Match             54.4%;  Score 13.6;  DB 21;  Length 50;
  Best Local Similarity   66.7%;  Pred. No. 1.5e+03;
  Matches   16;  Conservative    1;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       1 acagctcgcccccattaacatatt 24
           || |||||||||:  ||  |  ||
Db      42 ACCGCTCGCCCCSNNTAGGACTTT 19


RESULT  10
AAX36656
ID   AAX36656 standard; DNA; 20 BP.
XX
AC   AAX36656;
XX
DT   13-JUL-1999  (first entry)
XX
DE   PCR primer for marker D2S2181.
XX
KW   PCR primer; detection; glaucoma allele; haplotype analysis; human; GLC1B;
KW   chromosome 2; chromosome 6; GLC6p25; haplotype profile;
KW   presymptomatic glaucoma; symptomatic glaucoma; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9916899-A2.
XX
PD   08-APR-1999.
XX
PF   29-SEP-1998;   98WO-CA00924.
XX
PR   30-SEP-1997;   97CA-2217097.
XX
PA   (UYLA-) UNIV LAVAL.
XX
PI   Anctil J,  Cote G,  Falardeau P,  Morissette J,  Raymond V;
XX
DR   WPI; 1999-263704/22.
XX
PT   Haplotype analyses for indirect detection of glaucoma
XX
PS   Claim 7; Page 27; 41pp; English.
XX
CC   This sequence represents a PCR primer used in the method of the
CC   invention. The method is for detecting the presence of alleles for
CC   glaucoma comprising haplotype analysis of human chromosome 2 and 6
CC   respectively, where the haplotypes are associated with loci GLC1B and
CC   GLC6p25 respectively. The primers are used to amplify gene sequences to
CC   generate information necessary to compile haplotype profiles. The
CC   haplotype profiles can be used to detect presymptomatic and symptomatic
CC   glaucoma. They can also be used to localise, isolate and identify the
CC   GLC1B and GLC6p25 loci so that detection of individuals with glaucoma is
CC   enhanced. The haplotype analyses also provide means for identification
CC   and following of mutant alleles in pedigrees or populations.
CC   Identification of presymptomatic individuals using the methods allows
CC   intervention in the disease process and obviates the impact of inheriting
CC   a mutant allele causing disease, by medically disrupting the initiation
CC   or progression of the disease.
XX
SQ   Sequence 20 BP; 7 A; 6 C; 2 G; 5 T; 0 other;


  Query Match             53.6%;  Score 13.4;  DB 20;  Length 20;
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```
  Best Local Similarity   93.3%;  Pred. No. 1.6e+03;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      10 ccccattaacatatt 24
           ||||||||||| |||
Db       1 ccccattaacaaatt 15


RESULT  11
AAA73281
ID   AAA73281 standard; DNA; 29 BP.
XX
AC   AAA73281;
XX
DT   05-DEC-2000  (first entry)
XX
DE   A. fumigatus 13073 phytase mutagenesis primer SEQ ID NO:81.
XX
KW   Phytase; mutant; thermostability; mutation; mutagenesis; pH stability;
KW   temperature stability; pH profile; temperature profile; reaction rate;
KW   specific activity; substrate specificity; substrate cleavage pattern;
KW   substrate binding; position specificity; phytate degradation rate;
KW   food; feed; phytate; manure; PCR primer; ss.
XX
OS   Aspergillus fumigatus.
OS   Synthetic.
XX
PN   WO200043503-A1.
XX
PD   27-JUL-2000.
XX
PF   21-JAN-2000; 2000WO-DK00025.
XX
PR   22-JAN-1999;   99DK-0000092.
PR   21-SEP-1999;   99DK-0001340.
XX
PA   (NOVO ) NOVO NORDISK AS.
XX
PI   Lehmann M;
XX
DR   WPI; 2000-491161/43.
XX
PT   Novel phytases with improved properties such as temperature stability,
PT   pH stability and substrate specificity, for use in pharmaceuticals and
PT   compound foods and feeds -
XX
PS   Example 4; Page 45; 240pp; English.
XX
CC   The present invention describes improved phytases, preferably with
CC   increased thermostability, and methods for producing them. The methods
CC   can be used for producing phytases with improved properties e.g.
CC   temperature stability, pH stability, pH profile, temperature profile,
CC   specific activity, substrate specificity, substrate cleavage pattern,
CC   substrate binding, position specificity, the velocity and level of
CC   release of phosphate from corn, reaction rate, phytate degradation rate,
CC   and end level of released phosphate. The phytases can be used to produce
CC   pharmaceutical compositions or compound food or feeds. The feed can be
CC   used to reduce levels of phytate in animal manure, by converting it
CC   into lower inositol phosphates and/or inositol and inorganic phosphate.
CC   AAA73237 to AAA73289 represent phytase PCR primers and site-directed
CC   mutagenesis primers used in examples from the present invention.
XX
SQ   Sequence 29 BP; 6 A; 11 C; 6 G; 6 T; 0 other;


  Query Match           53.6%;  Score 13.4;  DB 21;  Length 29;
  Best Local Similarity   73.9%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       3 agctcgcccccattaacatattc 25
           |||||||| | |  | ||| |||
Db       7 agctcgcctcgagaagcatcttc 29
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```
RESULT  12
AAZ59726
ID   AAZ59726 standard; DNA; 29 BP.
XX
AC   AAZ59726;
XX
DT   19-APR-2000  (first entry)
XX
DE   Aspergillus fumigatus ATCC 13073 phytase A243L mutagenic PCR primer #1.
XX
KW   Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation;
KW   thermostable; animal feed; monogastric animal; phytate phosphorus;
KW   phosphate availibility; mutagenesis; PCR primer; ss.
XX
OS   Aspergillus fumigatus ATCC13073.
OS   Synthetic.
XX
PN   EP969089-A1.
XX
PD   05-JAN-2000.
XX
PF   23-JUN-1999;   99EP-0111949.
XX
PR   29-JUN-1998;   98EP-0111960.
XX
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Brugger R,  Lehmann M,  Wyss M;
XX
DR   WPI; 2000-099429/09.
XX
PT   New stabilized enzyme formulation, useful for feed compositions for
PT   monogastric animals -
XX
PS   Example 6; Page 25; 101pp; English.
XX
CC   The invention relates to a novel stabilised dry or liquid enzyme
CC   formulation, comprising phytase (myo-inositol hexakisphosphate
CC   phosphohydrolase) and one or more stabilising agents including
CC   xylitol or ribitol; polyethylene glycols with a molecular weight of 600
CC   to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of malonic,
CC   glutaric and succinic acid; carboxymethylcellulose; and sodium alginate.
CC   The stabilised phytase formulation is used in a method for preparing a
CC   feed composition for monogastric animals (e.g., pigs, poultry) and
CC   provides a monogastric animal with its dietary requirements of
CC   phosphorus. Although a large amount of phosphate is present in animal
CC   feed in the form of phytate phosphorus, monogastric animals are unable
CC   to utilise this form of phosphate, resulting in the addition of extra
CC   phosphate to the feed of such animals. Phytase enhances the nutritional
CC   value of plant material without the need for adding additional phosphate
CC   to the feed. The level of phosphate pollution in the environment is
CC   reduced by adding phytase to animal feed, as the animal can make use of
CC   the inorganic phosphate liberated from phytate phosphorus using the
CC   enzyme. The phytase formulation of the invention has an improved
CC   thermostability and can therefore remain stable during long-term storage
CC   and can withstand feed processing methods such as extrusion, expansion
CC   and pelleting. Sequences AAZ59618-Z59737 represent mutagenic PCR
CC   primers used to introduce mutations into DNA encoding Aspergillus
CC   fumigatus ATCC 13073 wild-type phytase (AAY69549) to create the more
CC   thermostable mutants a-mutant (AAY69570) and alpha-mutant (AAY69574).
XX
SQ   Sequence 29 BP; 6 A; 11 C; 6 G; 6 T; 0 other;


  Query Match           53.6%;  Score 13.4;  DB 21;  Length 29;
  Best Local Similarity   73.9%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       3 agctcgcccccattaacatattc 25
           |||||||| | |  | ||| |||
Db       7 agctcgcctcgagaagcatcttc 29
```

RESULT 13
AAZ59727/c
ID AAZ59727 standard; DNA; 29 BP.
XX
AC AAZ59727;
XX
DT 19-APR-2000 (first entry)
XX
DE Aspergillus fumigatus ATCC 13073 phytase A243L mutagenic PCR primer #2.
XX
KW Phytase; myo-inositol hexakisphosphate phosphohydrolase; stabilisation;
KW thermostable; animal feed; monogastric animal; phytate phosphorus;
KW phosphate availibility; mutagenesis; PCR primer; ss.
XX
OS Aspergillus fumigatus ATCC13073.
OS Synthetic.
XX
PN EP969089-A1.
XX
PD 05-JAN-2000.
XX
PF 23-JUN-1999; 99EP-0111949.
XX
PR 29-JUN-1998; 98EP-0111960.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Brugger R, Lehmann M, Wyss M;
XX
DR WPI; 2000-099429/09.
XX
PT New stabilized enzyme formulation, useful for feed compositions for
PT monogastric animals -
XX
PS Example 6; Page 25; 101pp; English.
XX
CC The invention relates to a novel stabilised dry or liquid enzyme
CC formulation, comprising phytase (myo-inositol hexakisphosphate
CC phosphohydrolase) and one or more stabilising agents including
CC xylitol or ribitol; polyethylene glycols with a molecular weight of 600
CC to 4000 Da, preferably 1000 to 3350 Da; the disodium salts of malonic,
CC glutaric and succinic acid; carboxymethylcellulose; and sodium alginate.
CC The stabilised phytase formulation is used in a method for preparing a
CC feed composition for monogastric animals (e.g., pigs, poultry) and
CC provides a monogastric animal with its dietary requirements of
CC phosphorus. Although a large amount of phosphate is present in animal
CC feed in the form of phytate phosphorus, monogastric animals are unable
CC to utilise this form of phosphate, resulting in the addition of extra
CC phosphate to the feed of such animals. Phytase enhances the nutritional
CC value of plant material without the need for adding additional phosphate
CC to the feed. The level of phosphate pollution in the environment is
CC reduced by adding phytase to animal feed, as the animal can make use of
CC the inorganic phosphate liberated from phytate phosphorus using the
CC enzyme. The phytase formulation of the invention has an improved
CC thermostability and can therefore remain stable during long-term storage
CC and can withstand feed processing methods such as extrusion, expansion
CC and pelleting. Sequences AAZ59618-Z59737 represent mutagenic PCR
CC primers used to introduce mutations into DNA encoding Aspergillus
CC fumigatus ATCC 13073 wild-type phytase (AAY69549) to create the more
CC thermostable mutants a-mutant (AAY69570) and alpha-mutant (AAY69574).
XX
SQ Sequence 29 BP; 6 A; 6 C; 11 G; 6 T; 0 other;

Query Match 53.6%; Score 13.4; DB 21; Length 29;
Best Local Similarity 73.9%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 agctcgcccccattaacatattc 25
|||||||| | | | ||| |||
Db 23 AGCTCGCCTCGAGAAGCATCTTC 1

RESULT 14
AAS05802
ID AAS05802 standard; DNA; 29 BP.
XX
AC AAS05802;
XX
DT 12-SEP-2001 (first entry)
XX
DE A. fumigatus site directed mutagenesis PCR primer A243L #1.
XX
KW PCR primer; fermentation; antibody; vaccine; antigen;
KW therapeutic protein; lactoternin; lactoperoxidase; lysozyme; ss;
KW antibacterial protein; thermostability; site directed mutagenesis;
KW 13073 phytase; A243L.
XX
OS Aspergillus fumigatus.
XX
PN EP1092764-A2.
XX
PD 18-APR-2001.
XX
PF 04-OCT-2000; 2000EP-0121663.
XX
PR 11-OCT-1999; 99EP-0120289.
PR 08-SEP-2000; 2000EP-0119676.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Bartok A, Mueh T, Rueckel M;
XX
DR WPI; 2001-309818/33.
XX
PT New fermentation assembly, useful for the continuous process of
PT manufacturing proteins, especially therapeutic proteins (e.g.
PT antibodies, vaccines or antigens), or antibacterial or
PT health-beneficial proteins (e.g. lactoternin) -
XX
PS Example 9; Page 22; 157pp; English.
XX
CC The sequence represents a site directed mutagenesis PCR primer used
CC to mutate a nucleic acid molecule encoding 13073 phytase (a
CC phytase used to demonstrate the process of the invention) at
CC a position in the mature phytase-1, A243L, in order to make 13073
CC resemble more closely the consensus phytase. The invention relates to a
CC fermentation assembly comprising a vessel for carrying out reactions
CC involving living cells, at least two storage flasks connected to the
CC vessel for supply of liquids (including means to transport the liquids
CC from the storage flasks to the vessel), individual appliances monitoring
CC the supply of the contents of the storage flasks to the vessel, a harvest
CC flask connected to the vessel (including means to transport fermentation
CC broth from the vessel to the harvest flask) and a device for controlling
CC and maintaining a constant dilution rate in the vessel with varying rates
CC of individual supply of liquid from the storage flasks to the vessel. The
CC process is also envisaged to included a continuous process for
CC manufacturing proteins from cultures of living cells. In the process, the
CC nutrients and other agents required for the growth of the cells and the
CC optimal production of the desired protein are fed into the reactor
CC individually at a constant dilution rate. The fermentation assembly is
CC useful for the continuous process of manufacturing proteins, especially
CC therapeutic proteins (e.g. antibodies, vaccines or antigens) or
CC antibacterial and/or health-beneficial proteins (e.g. lactoternin,
CC lactoperoxidase or lysozyme) and phytases (including mutants with altered
CC thermostability and pH tolerance).
XX
SQ Sequence 29 BP; 6 A; 11 C; 6 G; 6 T; 0 other;

Query Match 53.6%; Score 13.4; DB 22; Length 29;
Best Local Similarity 73.9%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 agctcgcccccattaacatattc 25

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          ||||||||| | |  | ||| |||
Db      7 agctcgcctcgagaagcatcttc 29
```

RESULT 15
AAS05803/c
ID AAS05803 standard; DNA; 29 BP.
XX
AC AAS05803;
XX
DT 12-SEP-2001 (first entry)
XX
DE A. fumigatus site directed mutagenesis PCR primer A243L #2.
XX
KW PCR primer; fermentation; antibody; vaccine; antigen;
KW therapeutic protein; lactoternin; lactoperoxidase; lysozyme; ss;
KW antibacterial protein; thermostability; site directed mutagenesis;
KW 13073 phytase; A243L.
XX
OS Aspergillus fumigatus.
XX
PN EP1092764-A2.
XX
PD 18-APR-2001.
XX
PF 04-OCT-2000; 2000EP-0121663.
XX
PR 11-OCT-1999; 99EP-0120289.
PR 08-SEP-2000; 2000EP-0119676.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Bartok A, Mueh T, Rueckel M;
XX
DR WPI; 2001-309818/33.
XX
PT New fermentation assembly, useful for the continuous process of
PT manufacturing proteins, especially therapeutic proteins (e.g.
PT antibodies, vaccines or antigens), or antibacterial or
PT health-beneficial proteins (e.g. lactoternin) -
XX
PS Example 9; Page 22; 157pp; English.
XX
CC The sequence represents a site directed mutagenesis PCR primer used
CC to mutate a nucleic acid molecule encoding 13073 phytase (a
CC phytase used to demonstrate the process of the invention) at
CC a position in the mature phytase-1, A243L, in order to make 13073
CC resemble more closely the consensus phytase. The invention relates to a
CC fermentation assembly comprising a vessel for carrying out reactions
CC involving living cells, at least two storage flasks connected to the
CC vessel for supply of liquids (including means to transport the liquids
CC from the storage flasks to the vessel), individual appliances monitoring
CC the supply of the contents of the storage flasks to the vessel, a harvest
CC flask connected to the vessel (including means to transport fermentation
CC broth from the vessel to the harvest flask) and a device for controlling
CC and maintaining a constant dilution rate in the vessel with varying rates
CC of individual supply of liquid from the storage flasks to the vessel. The
CC process is also envisaged to included a continuous process for
CC manufacturing proteins from cultures of living cells. In the process, the
CC nutrients and other agents required for the growth of the cells and the
CC optimal production of the desired protein are fed into the reactor
CC individually at a constant dilution rate. The fermentation assembly is
CC useful for the continuous process of manufacturing proteins, especially
CC therapeutic proteins (e.g. antibodies, vaccines or antigens) or
CC antibacterial and/or health-beneficial proteins (e.g. lactoternin,
CC lactoperoxidase or lysozyme) and phytases (including mutants with altered
CC thermostability and pH tolerance).
XX
SQ Sequence 29 BP; 6 A; 6 C; 11 G; 6 T; 0 other;

Query Match 53.6%; Score 13.4; DB 22; Length 29;
Best Local Similarity 73.9%; Pred. No. 1.7e+03;

Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy      3 agctcgcccccattaacatattc 25
          ||||||||| | |  | ||| |||
Db     23 AGCTCGCCTCGAGAAGCATCTTC 1
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